SEQUENCE LISTING

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     YASOHARA, YOSHIHIKO
     HASEGAWA, JUNZO

<120> NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

<130> 025835/0104

<140> 10/088,920
<141> 2002-06-03

<150> PCT/JP01/06619
<151> 2001-08-01

<150> JP 2000-232756
<151> 2000-08-01

<160> 11

<210> 1
<211> 277
<212> PRT
<213> Micrococcus luteus

<400> 1
Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly
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Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu
            20   25   30

Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp
            35   40   45

Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu
    50   55   60

Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met
 65   70   75   80

Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser
            85   90   95

Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp
            100   105   110

Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu
            115   120   125

Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His
    130   135   140

Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr
145   150   155   160

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        Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp
                        165                 170                 175

        Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser
                        180                 185                 190

        Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val
                        195                 200                 205

        Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val
                210                 215                 220

        Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
        225                 230                 235                 240

        His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
                        245                 250                 255

        Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
                        260                 265                 270

        Pro Leu Glu Met Leu
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<210> 2
<211> 1410
<212> DNA
<213> Micrococcus luteus

<220>
<221> CDS
<222> (108)..(938)

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ctcagcccac gtcccgcctc aggacaacca gaaggaagtg atcgcgg atg cga cgg     116
                                                    Met Arg Arg
                                                     1

atg acg ctg ccg agt ggg gag tcc atc cct gtg ctg ggc cag ggc acc     164
Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly Gln Gly Thr
      5                  10                  15

tgg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag gtc gcc gcg     212
Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu Val Ala Ala
 20                  25                  30                  35

ctg cac gcc ggc ctc gag ctg ggc atg acg ctg gtc gac acc gcc gag     260
Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp Thr Ala Glu
                40                  45                  50

atg tac gcc gac ggc ggt gcg gag gag gtg gct ggt gaa gca ttg gcg     308
Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu Ala Leu Ala
                55                  60                  65
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ggt cgc cgc gac gag gcg ttc gtg gtc agc aag gtc atg ccg tcc cac      356
Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met Pro Ser His
        70                  75                  80

gcc tcc cgt tcc ggc acg atc gcg gcc tgc gaa cgc agc ctg aaa cgc      404
Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser Leu Lys Arg
        85                  90                  95

ctg ggc acc gat cgg atc gac ctc tac ctg ctg cac tgg cag ggc agg      452
Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp Gln Gly Arg
100                 105                 110                 115

tac ccg ctg cag gac acc gtc gcg gcc ttc cac cag ctc gtc gag gac      500
Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu Val Glu Asp
                120                 125                 130

ggg aaa atc cga tac tgg ggc gtc agc aac ttc gac cac cgg gcc ctc      548
Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His Arg Ala Leu
                135                 140                 145

gcc gag ctg cag gac gtg ccg ggc acc agc ggg ctg acc acg gat cag      596
Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr Thr Asp Gln
                150                 155                 160

gtg ctg tac aac ctg tcg cgg cga gga ccg gag tac gac ctg ctg ccg      644
Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp Leu Leu Pro
    165                 170                 175

tgg tgc gcc gac cac cag ctg ccg gtc atg gcg tac tcg ccg atc gag      692
Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser Pro Ile Glu
180                 185                 190                 195

cag ggc cgc atc ctt gac gac acg acg ctg aac gac gtc gcg gcc cgt      740
Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val Ala Ala Arg
                200                 205                 210

cac agc gtc agc ccc gcg gcg gcg gcc ctt gcc tgg gtg ctg cgc cgc      788
His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val Leu Arg Arg
                215                 220                 225

gac tcg ctc tgc acg atc ccc aag gcg agc agc ccg cag cac gtg cgc      836
Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln His Val Arg
                230                 235                 240

gac aac gcc aca gca ctg gac gtg gag ctg acc cgc gaa gac ctg gat      884
Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu Asp Leu Asp
    245                 250                 255

gct ctg gac cgt gcg ttt ccg ccc ccg agc gga ccg cga cca ctg gaa      932
Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg Pro Leu Glu
260                 265                 270                 275

atg ctg tgaccctgcc ccagggcgca gcccggtcgg tccgggcggt ccgggcagtc      980
Met Leu

cgggcagcgc tccggtcagc gcaagtctcc gaaggacctg cctgtcacct cctcctgaac     1048

ctgtgcacgc catccatcga ctcctttcct cgagccctgt cgggttcgcg gtaggcgctg     1108
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atcatccgct ggcaggtccc ccaagtggcc tcgagccggg ccctctgctt gtcggtgagc 1168

aacccggttc cggcgtgcag ggttcgacgg gcggagtaga gcgggtcgcc cgtgcggccg 1228

cggtggccat gcaggtcctg ctggacccgg cggtggcagc ggaccaacgc gtcgccggct 1288

aaccggactg cgagcgaccg gcgttgtgga cgcagacgac ctggacactg ggccgtgcgg 1348

tcaggaggat ctccaaagtc ggcggcgggg gttcaggcga tgtcgaggaa ggaacggagc 1408

tc   1410

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (6)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (9)
<223> a, t, c, g, other or unknown

<400> 3
gayacngcng aratgtaygc   20

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
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<223> a, t, c, g, other or unknown

<220>
<221> modified_base
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<223> a, t, c, g, other or unknown

<400> 4
tcytcnacna gytgrtgraa   20

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gcgcatatgc gacggatgac gctgcc   26

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
ggcgaattct tacagcattt ccagtggtcg cg   32

<210> 7
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gcgaattcta aggagattta tatatgcgac ggatgacgct gccgag   46

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
caggagctct tacagcattt ccagtggtc   29

<210> 9
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      double-stranded DNA

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<400> 9
gaattctaag gagatttaca tatgcgtcgt atgactttac catctggtga atctattcca    60
gttttaggtc aaggtacttg gggttggggt gaagatccag gtcgtcgtgg tgatgaagtt   120
gctgctttac atgctggtct cgag                                         144


<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
caggagctct aaggaggtta acaatgtata aag                                33


<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
cacggatcct tatccgcgtc ctgcttgg                                      28
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